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57

Name : AFAF ROZAN MOHD RADZOL

Title : SALIVARY BASED SERS ANALYSIS IN RECOGNITION OF NS1 FOR PCA-SVM CLASSIFICATION OF DENGUE FEVER

Supervisor : ASSOC. PROF. DR. LEE YOOT KHUAN (MS)
ASSOC. PROF. DR. DATIN WAHIDAH MANSOR (CS)

NS1 is one of the seven non-structural proteins encoded in the RNA of flavivirus genome. It has been recognized as an early biomarker for flavivirus infection diseases. In the case of DF, NS1 is detectable in patients' blood serum from day 1 to 9 before the formation of IgM and IgG antibodies. ELISA is the most common technique used to detect NS1 from patients' blood serum. However, this technique suffers from limitations such as being invasive, delayed diagnosis, tedious sample preparation, in need of seasoned laboratory, technician and bulky expensive laboratory equipment. The presence of NS1 in blood can also be detected using immune-chromatic strip. While portable, this technique suffers from disadvantages such as non-type-specific, un-validated diagnostic accuracy, non-cost effective in addition to limitations mentioned before. Recently, the presence of NS1 in saliva via ELISA has been reported, but with low sensitivity (64.7%). SERS is a form of Raman spectroscopy which can provide fingerprint spectra, unique of each molecule at a higher signal intensity. It has been applied to detect a variety of diseases. Yet, its being used to identify NS1 molecule in saliva of DF patients remains unexplored. From SERS analysis, NS1 protein has been proven to be Raman active. It is found to produce a molecular fingerprint with a distinct characteristic peak at 1000cm-1. This peak is then chosen as the marker for automated classification algorithm for detecting NS1 in saliva. This study intends (i) to establish Raman fingerprint of NS1; (ii) to design algorithms for optimal classification of positive and negative DF subjects from salivary Raman spectra; (iii) to benchmark performance of optimised classifiers against two recommended serological diagnostic tests by WHO, NS1-ELISA and NS1-Rapid. Saliva samples from healthy and suspected dengue patients are collected and analysed using SERS technique to obtain the salivary Raman spectra. The spectra are pre-processed to remove unwanted features using signal processing algorithms customized and optimized for this study. Then, the clean spectra are analysed using PCA for feature extraction and dimension reduction. Finally, the extracted principal components are classified into dengue positive and negative using SVM algorithm. NS1 ELISA and NS1 Rapid serum tests result are used as benchmark against sensitivity, specificity and accuracy performance of the SVM algorithms in which three types of kernels i.e; Linear, RBF and MLP are optimized and compared. From the results, it is observed that RBF kernel gives the best performance. The highest performance of SVM-RBF classifier against NS1-ELISA benchmark is [83.22%, 88.27%, 78.13%] using 95 principal components proposed by CPV criterion, while the highest performance against NS1-Rapid benchmark is [81.90%, 80.32%, 83.49%] using 110 principal components proposed by Kaiser criterion. Both performances achieved is found better than detection of NS1 in saliva using ELISA technique by researchers for acute cases with performance of [NA, 64.7%, 95.8%]. The finding supports that SERS technique integrated with signal processing techniques is sensitive to detect the presence of NS1 in saliva.